

**Amendments to the Claims:**

1-26. (Cancelled)

27. (Currently amended) A polynucleotide comprising a sequence of at least 7 nucleotides that specifically hybridizes to a first nucleotide sequence within an accessible region of the RNA component of a human telomerase (hTR), wherein said polynucleotide ~~but that~~ does not hybridize to a second nucleotide sequence within a template region of the hTR, and wherein the ~~first nucleotide sequence within an~~ accessible region is selected from the group consisting of nucleotides 137-196, nucleotides 290-319, and nucleotides 350-380 of hTR (SEQ ID NO:16),

and wherein the polynucleotide comprises a nucleotide analog or a non-naturally occurring nucleotide analog linkage selected from the group consisting of phosphorothioates, phosphoramidates, methyl phosphonates, chiral-methyl phosphonates, 2-O-methyl ribonucleotides and peptide-nucleic acids,

and wherein the polynucleotide is effective to inhibit the synthesis of telomeric DNA by telomerase.

28. (Currently amended) A polynucleotide ~~according to claim 27 comprising a sequence of at least 7 nucleotides that specifically hybridizes to a first nucleotide sequence within an accessible region of the RNA component of a human telomerase (hTR), said region selected from the group consisting of nucleotides 137-196, nucleotides 290-319, and nucleotides 350-380 of SEQ ID NO:16,~~

wherein:

said polynucleotide does not hybridize to a nucleotide sequence within a template region of the hTR; when

the polynucleotide sequence is selected from the group consisting of:

CGT TCC TCT TCC TGC GGC CTG AAA CGG (SEQ ID NO:2)

CGT TCC TCT TCC TGC GGC CT (SEQ ID NO:3)

CGT TCC TCT TCC (SEQ ID NO:4)

CTG ACA GAG CCC AAC TCT TCG CGG TGG CAG (SEQ ID NO:5)

CTG ACA GAG CCC AAC TCT TC (SEQ ID NO:6)

CCA ACT CTT CGC GGT GGC AG (SEQ ID NO:7)

GCT CTA GAA TGA ACG GTG GAA GGC GGC AGG (SEQ ID NO:8)

GCT CTA GAA TGA ACG GTG G (SEQ ID NO:9)

GCT CTA GAA TGA ACG (SEQ ID NO:10)

GCT CTA GAA TG (SEQ ID NO:11)

GCT CTA G (SEQ ID NO:12)

CAT TTT TTG TTT GCT CTA GA (SEQ ID NO:13) and

CGG GCC AGC AGC TGA CA (SEQ ID NO:14); and

the polynucleotide comprises a nucleotide analog or a non-naturally occurring nucleotide analog linkage selected from the group consisting of phosphorothioates, phosphoramidates, methyl phosphonates, chiral methyl phosphonates, 2'-O-methyl ribonucleotides, and peptide nucleic acids.

29. (Currently amended) A polynucleotide consisting ~~essentially~~ of a sequence selected from the group consisting of:

CGT TCC TCT TCC TGC GGC CTG AAA CGG (SEQ ID NO:2)

CGT TCC TCT TCC TGC GGC CT (SEQ ID NO:3)

CGT TCC TCT TCC (SEQ ID NO:4)

CTG ACA GAG CCC AAC TCT TCG CGG TGG CAG (SEQ ID NO:5)

CTG ACA GAG CCC AAC TCT TC (SEQ ID NO:6)

CCA ACT CTT CGC GGT GGC AG (SEQ ID NO:7)

GCT CTA GAA TGA ACG GTG GAA GGC GGC AGG (SEQ ID NO:8)

GCT CTA GAA TGA ACG GTG G (SEQ ID NO:9)

GCT CTA GAA TGA ACG (SEQ ID NO:10)

GCT CTA GAA TG (SEQ ID NO:11)

GCT CTA G (SEQ ID NO:12)

CAT TTT TTG TTT GCT CTA GA (SEQ ID NO:13) and

CGG GCC AGC AGC TGA CA (SEQ ID NO:14).

30. (New) The polynucleotide of claim 28, wherein said polynucleotide comprises a sequence of at least 7 nucleotides that specifically hybridizes to a first nucleotide sequence within an accessible region of the RNA component of a human telomerase (hTR), said accessible region being nucleotides 137-196 of SEQ ID NO: 16.

31. (New) The polynucleotide of claim 30, wherein said accessible region is nucleotides 137-166 of SEQ ID NO: 16.

32. (New) The polynucleotide of claim 28, wherein said polynucleotide comprises a sequence of at least 7 nucleotides that specifically hybridizes to a first nucleotide sequence within an accessible region of the RNA component of a human telomerase (hTR), said accessible region being nucleotides 290-319 of SEQ ID NO: 16.

33. (New) The polynucleotide of claim 28, wherein said polynucleotide comprises a sequence of at least 7 nucleotides that specifically hybridizes to a first nucleotide sequence within an accessible region of the RNA component of a human telomerase (hTR), said accessible region being nucleotides 350-380 of SEQ ID NO: 16.